

Fig. 1

SEG 10 No: 8

5'	GGGGGGGGGGAACAGGAGCAGCAGAACTCAAGAGAAAGCCAACTCTCAACGATTGTCTGCCAATTGAACCACTTTATCC	81
ATCCTCTGCCTCCCCGAGACCCAGAAGAAG	ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC	152
Seq ID No. 3	Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu	-88
TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG		214
Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu		-67
CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG		272
Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu		-46
CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC		340
Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly		-25
GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT		403
Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg		-4
GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC		466
Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys ***		
CTTTACTGTGTGTAACATCTCATCTCTTTTGTTCATCACTCATTGCTGAATCCAATGCACCATGGCCTAACCCCTCTCT		549
TCAAAAAATTTAAATAAACACTGTTATACTTTAAACAATCATTCTGATGTTTCTATCGCTCACTTAGATTTTTTCCGAAAAG		632
GAACACAAGAAGAATGTTCTCAAAATGTAATGCGGTTCTGCTTTGACGTGATTTATGTATTTTGGCAGACTATTTTAATTG		715
TTTGTGTTGAATAAAATCTGTGTTTCAGAACCAAAAAAAAAAAAAA	3'	

Fig. 2

[illegible]

PPSS-II' and PPSS-II''

SEQ ID NO: 14 PPSS-II' accaggcctgctccataaccgactgacccagatcgagcatagcccggtccagctcagctcgtctcaccgctgcca 75
PPSS-II'' accaggcctgctccataatcaactgatctagatccagcacaccccggtccagcttagctc*****accgtgctctgg 70

SEQ ID NO: 20 PPSS-II' tccctgcaaaccacacccagctctgttggag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC 139/-91
PPSS-II'' tccctgcaaaccacacccagctctgttggag ATG AGG GTC TCC CAA ATC CAC TGT GCA CTG GCC 134/-87

SEQ ID NO: 9 Lys Cys Arg
PPSS-II' CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCC GAC CTG 196/-72
PPSS-II'' CTG CTG GGT TTG GCC CTG GCA ATT TGC AGC CAA GGA GCC GCC TCG CAG CCA GAC CTG 191/-68
Leu Leu Gly Leu Ala Leu Ala Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu

Arg Arg
PPSS-II' GAC CTC CGC AGC CGC AGA CTC CTT CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG 253/-53
PPSS-II'' GAC CTC GCG AGC CGC CGA CTC CTC CAG AGG GCC CTG GCC GCT GCA TTG CCA CAC AGG 248/-49
Asp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Ala Ala Leu Pro His Arg

PPSS-II' AGT GGA GTA AGC GAG CGG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG *** *** 304/-35
PPSS-II'' AGT GGA GTA AGC GAG CGA TGG AGG ACA TTC TAT CCG AAC TGT CCT TGC CTG AGG TGG 305/-30
Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp

Cys Ala Gly Leu Arg Val Glu
PPSS-II' AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG 358/-18
PPSS-II'' AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** *** *** *** 350/-14
Arg Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp

PPSS-II' CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC 415/+2
PPSS-II'' CTG GAG CGC TCA GTG GAC *** *** *** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC 398/+2
Leu Glu Arg Ser Val Asp Asn Leu Pro Pro Arg Glu Arg Lys Ala Gly

PPSS-II' TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga gggaagaataaaccgaccacett 477
PPSS-II'' TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TGC taa gggaagaaaagcctgaccacett 460
Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ###

PPSS-II' atgacatgacgctgccaatcacgtcacaccgccaacttaacacctgaagaaatgcagccaatcaacagttagctgtg 552
PPSS-II'' atgacacaatgcattcaatcacatcacaccgccaacettctctgactaatgttagccaatcagcaattagctgtg 535

PPSS-II' cccgatgatggttcttgaatcaacagaatgatgtacctgtctaatattgtgaaataaataatataataaattg(a)n
PPSS-II'' cctgatgacaattatgattatgatgtacctgactaatttagaataaagagaaataaagagaaac(a)n

Fig. 3

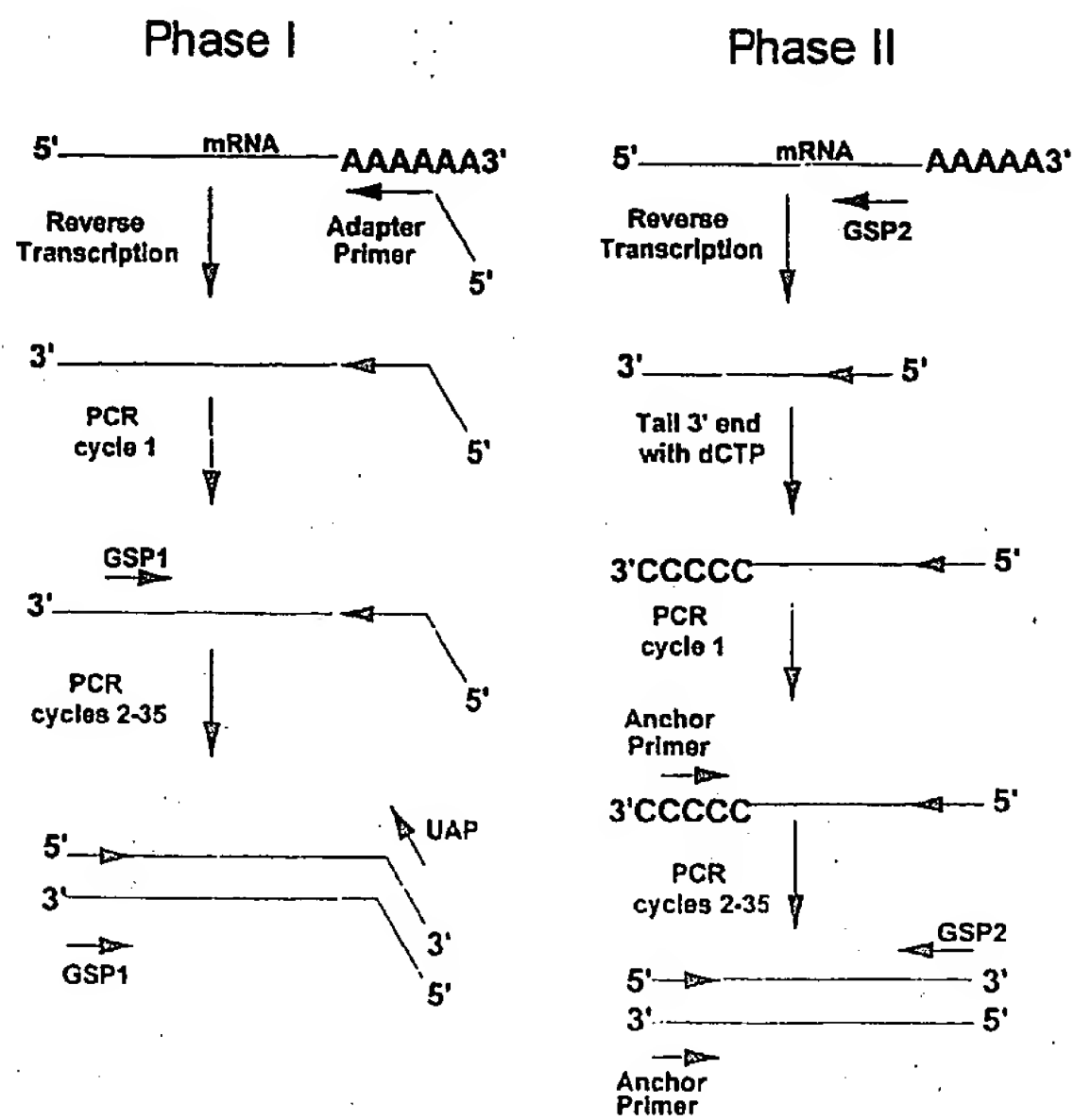


Fig. 4

Fig. 5

12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100											
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin 1^a

	-20	-10	+1	+10	+14
Rainbow trout ^b			APG**PVLAPRERK	AGCKNFFFWK	TFTSCSEQIDNO:4
Hagfish ^d	AVERPRQDGGQVHEPPGRERK			AGCKNFFFWK	TFTSCSEQIDNO:27
Lamprey ^d				AGCKNFFFWK	TFTSCSEQIDNO:1
Torpedo ^d				AGCKNFFFWK	TFTSCSEQIDNO:1
Ratfish ^d				AGCKSFFFWK	TFTSCSEQIDNO:28
Bowfin ^d			SAN**PALAPRERK	AGCKNFFFWK	TFTSCSEQIDNO:29
Sturgeon ^d				APCKNFFFWK	TFTSCSEQIDNO:30
Catfish ^d				AGCKNFFFWK	TFTSCSEQIDNO:1
Salmon ^d				AGCKNFFFWK	TFTSCSEQIDNO:1
Anglerfish ^c			AASGGPLLA PRERK	AGCKNFFFWK	TFTSCSEQIDNO:31
Eel ^d				AGCKNFFFWK	TFTSCSEQIDNO:1
Flounder ^d				AGCKNFYWK	GFTTSCSEQIDNO:2
Sculpin ^d				AGCKNFYWK	GFTTSCSEQIDNO:2
Frog ^c				AGCKNFFFWK	TFTTSCSEQIDNO:1
Salamander ^d				AGCKNFFFWK	TFTTSCSEQIDNO:1
Alligator ^d				AGCKNFFFWK	TFTTSCSEQIDNO:1
Pigeon ^d				AGCKNFFFWK	TFTTSCSEQIDNO:1
Ovine ^d			SANSNPAMAPRERK	AGCKNFFFWK	TFTTSCSEQIDNO:32

9
5
4

SEQ ID NO: 9	TRII'	---MKVCRTHCALALLGLALATCSQGAASQP	---DLDRSRRLTORARAAWPHRSGVSER
SEQ ID NO: 15	TRII"	---MRVSOITHCALALLGLALATCSQGAASQP	---DLDRASRRILORALAAALPHRSGVSER
SEQ ID NO: 36	CFII	---MSSSPLRLALATMCIVSAVGVTISCGRP	---HVVLNSAHNEEARNVPFGEEVPERLT
SEQ ID NO: 37	AFII	---MQCTRCPAIDALLALVLCGPSVSSOLDREQSDNQDLDLELROIWITERARSAGLLSQEWSKRA	
SEQ ID NO: 38	GFII	---MRLCELHCYATIGESVLGRCANSOL	---EP---DLDFRHHRLLEORASATGOATQDFTKRD
SEQ ID NO: 39	GFIII	---MQLSSDVSLVLVLYSVRAAVL	---PVEERNPAQSRELSKE-RKELILKL
SEQ ID NO: 40	FRII	---MLGSAGTELELLLLAW-GARALSO	---PDONRITTGRNQDLNAIQQDLLLLKL
SEQ ID NO: 3	TRI	---MLSTRVOCALALLSLALATSSVSAAPS	---DAKLROQLORSIMAPAGKQELARNT
SEQ ID NO: 41	CFI	---MPSTRIOCALALLAVALSVCSVSGAPS	---DAKLROQLORSILAPSVKQELTRYT
SEQ ID NO: 42	AFI	MKMVSSSRRLRCLLVLLLSLTASISCSFAGQR	---DSKLRLLLHRYPLOGS-KQDMTRSA
SEQ ID NO: 43	GFI	---MLSTRIOCALALLSLALAVCSVSAAPT	---DAKLROQLORSLLNPAGKQELARYT
SEQ ID NO: 44	FRI	---MQSCRVOCAITLISLALAINSISAAPT	---DPRLRQFLOKSLASAG-KQELAKYF
SEQ ID NO: 45	C	---MLSCRLOCALAALLSIALAVGTVSAAPS	---DPRLRQFLOKSLAAAGKQELAKYF
SEQ ID NO: 46	R	---MLSCRLOCALAALCIVLALGGVTGAPS	---DPRLRQFLOKSLAAATGKQELAKYF
SEQ ID NO: 47	B	---MLSCRLOCALAALSIVLALGGVTGAPS	---DPRLRQFLOKSLAAAGKQELAKYF
SEQ ID NO: 48	M	---MLSERLOCALAALSIVLALGCVTGAPS	---DPRLRQFLOKSLAAAGKQELAKYF
SEQ ID NO: 49	H	---MLSCRLOCALAALSIVLALGCVTGAPS	---DPRLRQFLOKSLAAAGKQELAKYF

(continued)

WRTEYPNCPCLR--PRKVKCP-AGAKE-DLR--VELERSVGN-PNNLPPRRERKAGCKNEYWKGETSC
WRTEYPNCPCLRWRPRKVKGPOLKAKE-DL-----ERSV---DNLPPRRERKAGCKNEYWKGETSC
LPELQW-MLSNNELTPVQVEEAPRS-----RLELVRRDN-----T-VTSKPLNEMNYFWKSRDAG
VEELLAQMSLPEATFORAEDASMATE-G---RMNLEERSVDS-TNNLPPRRERKAGCKNEYWKGETSC
VEKLLSLLSIPEMEMR--EKGLSMAGE-SEDLRLEQERSAES-SNOLPTRVRKEGCKNEYWKGETSC
ISGLLD--GVDNSVLDGEIAPVPFDAAEFLESRL-ERAVYNRLSOLPORORKAPEKNEFWKTETSC
LSGWTD--S-RESNLVEVERNVPDPPE-P-----KIPPSVK--FPRSLRERKAPCKNEFWKTETMC
LVLLS-ELAHYVENEAIELDDMSHGVE-QEDVLELERAPG---PVLAPRERKAGCKNEFWKTETSC
LAELLA-ELAEAENEVLDSDEVSPAAE-SEGARLEMBRAAG---PMLAPRERKAGCKNEFWKTETSC
LAELLI.SDLOGENEALEEENFPLAEGGPEDAHADLERAASG-GPLLAPRERKAGCKNEFWKTETSC
LADLLS-ELVQAENEALEPEDLSRAVE-KDEVRLERLERAAG---PMLAPRERKAGCKNEFWKTETSC
LAELLS-EPSTQDNEALESDDLPRGAE-QDEVRLERLERSANS-SPALAPRERKAGCKNEFWKTETSC
LAELLS-EPSTQDNEALESDDLPRGAE-QDEVRLERLERSANS-NPAMAPRERKAGCKNEFWKTETSC
LAELLS-EPNQTENDALEPEDLPOAAE-QDEMRLERLORSANS-NPAMAPRERKAGCKNEFWKTETSC
LAELLS-EPNQTENDALEPEDLPOAAE-QDEMRLERLORSANS-NPAMAPRERKAGCKNEFWKTETSC
LAELLS-EPNQTENDALEPEDLPOAAE-QDEMRLERLORSANS-NPAMAPRERKAGCKNEFWKTETSC
LAELLS-EPNQTENDALEPEDLPOAAE-QDEMRLERLORSANS-NPAMAPRERKAGCKNEFWKTETSC
LAELLS-EPNQTENDALEPEDLPOAAE-QDEMRLERLORSANS-NPAMAPRERKAGCKNEFWKTETSC

Fig. 7

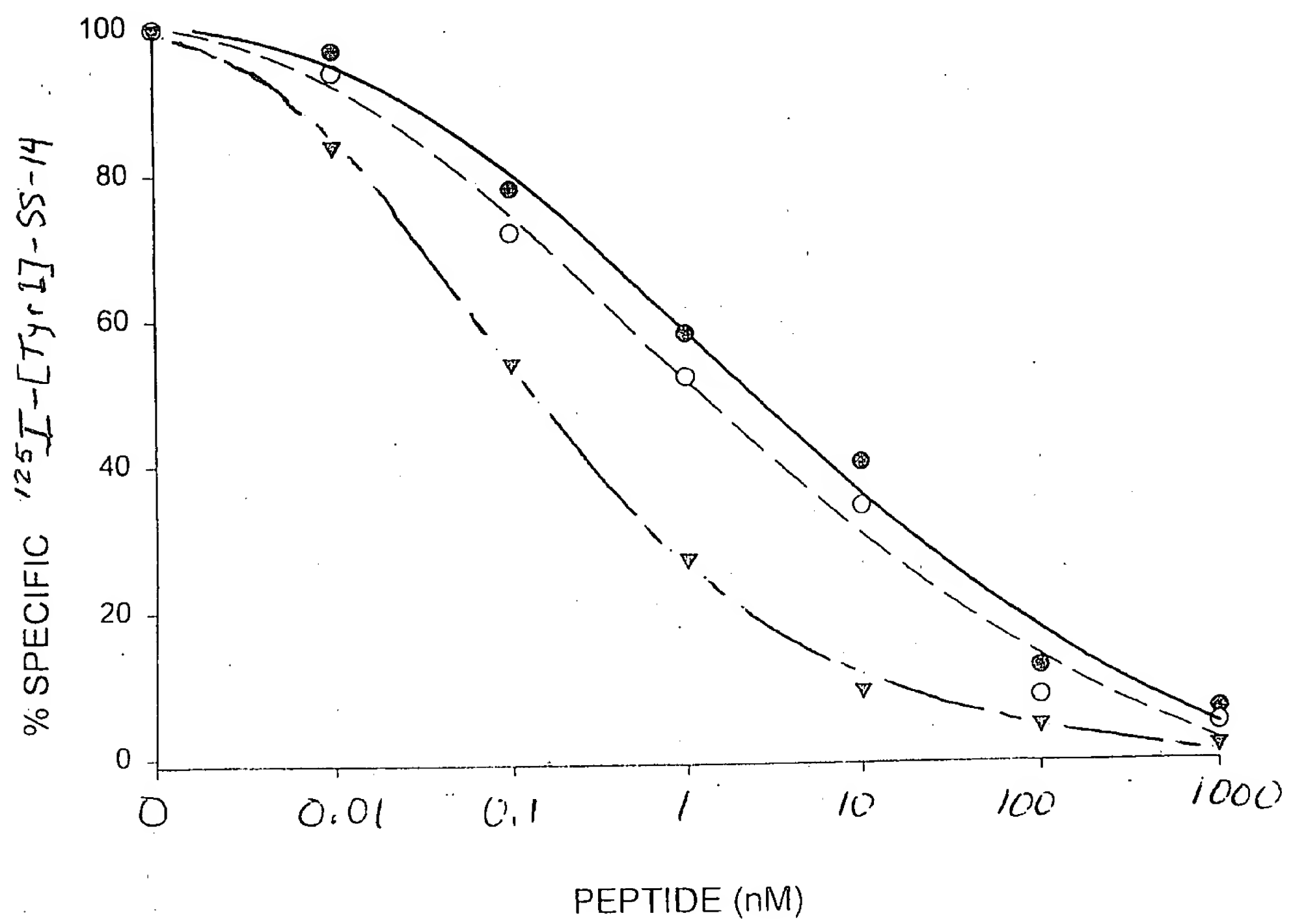


Fig. 8